

Inventor: Bryan JULIEN

Title: TRANSFORMATION SYSTEM BASED ON THE INTEGRASE GENE
AND ATTACHMENT SITE FOR MYXOCOCCUS XANTHUS
BACTERIOPHAGE MX9

Sheet 1 of 12

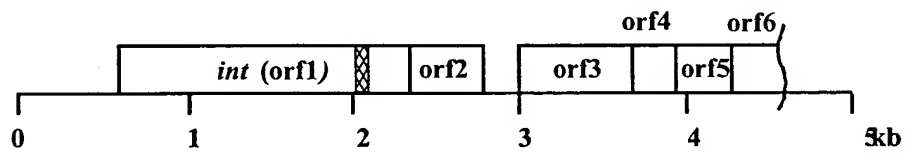


Figure 1

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Figure 2

10	20	30	40	50	60	70	80	90	100	110	120
GTGGCGCTCAGGGGTGGTGGACGCCACTACCAACCCCTCTCGACTTGTGCAGTTCGTCCCGCGCGCGTGGCGACTCCGTGGGGTGTTCAGTGGCTCGTGGTACCTGTAGGCGGT	20	30	40	50	60	70	80	90	100	110	120
JACACCGCGAGTCCCAAGCAGCGCTGGGTGATGTGTGGGAGAGCTGAACCTCAGCAGCGCGCGCGCGCGCGTGAAGCACCCACAGTACGCAGCACCATGGAGCATCCCGCA	20	30	40	50	60	70	80	90	100	110	120
V A L R G A S D A T T N P S R L V Q S V A A G P R A T P W G V S A S W Y L L G R	20	30	40	50	60	70	80	90	100	110	120
130	140	150	160	170	180	190	200	210	220	230	240
ACACAGACGGGGAGTATCATCGTGTAGTAGCAGCGCGGGAAGAGGGCCATCCAATGGCGCACTGCGGCGGAGCGGTTGCCGAGCTACCAATCGACGTCAACGCTCTGGCGCTGTGAGGTG	130	140	150	160	170	180	190	200	210	220	230
TTGTGTGTTGCCCTCATGTAGCACTCATCGCTGCGCGCTTCTTCCGGTAGGTACCGTTAGCGCGCTCGCCAAACGCTGCGAGTGGTGTAGTGTAGTGTGGAGACCGGAGCTCCGCA	130	140	150	160	170	180	190	200	210	220	230
T A T G E Y I V S S D A A K K G H P M A T A A E R L P T S P I D V N A L A L E V	130	140	150	160	170	180	190	200	210	220	230
250	260	270	280	290	300	310	320	330	340	350	360
CGGCGCGGCTTGGCCCTCCAGCAGCAAGTGCAGCGCGCCCATCGTCGCGCGCGCACTTTCGCGCGGTGGCGGATGACTGGGCTCATCTAGGCGCAAGCGCTCGTGTGCCCGCGCAAT	250	260	270	280	290	300	310	320	330	340	350
CGGCGCGAACAACGGGAGGTCTGTTCACTGCGGCGGTAGCAGCGCGGTGAAGCGCGCCACTACTGACCGAGTAGTGACTCCGGTTTCGGGAGCACACCGGGGCTGTTA	250	260	270	280	290	300	310	320	330	340	350
A R L V A L Q Q S A T P P S S G R T F G A V A D D W L I T E A K R L V C P D N	250	260	270	280	290	300	310	320	330	340	350
370	380	390	400	410	420	430	440	450	460	470	480
GAGCGCGCCCATCTTCGCCATATGAGGCGCTCTGGGCGATGACGAGTGTGAGTCTACGCGCGCGCTCGTGAAGCGCACTTCGGCGGACTTCTCAAGCCAGAGGGGCGCTGAGCGCA	370	380	390	400	410	420	430	440	450	460	470
CTTCGCGCGGTAGAACGGGTATACCTCCGCGAGACCCGTACTGCCTACACTCGAGTGCAGCGCACTTCGCGGTGGAACCGCTGAAGAGTTTCGTTCTCCCGCGGCACTCCGCT	370	380	390	400	410	420	430	440	450	460	470
E R R H L R H M E A L W G M T D V E L T P R V V K A H L A G L L K P E G P L S A	370	380	390	400	410	420	430	440	450	460	470
490	500	510	520	530	540	550	560	570	580	590	600
GGCCACCGTCAATAAGTGGCTCTACCGCAAGCGCATCATCAAGGCGCGCAATCAACGCGAGTGGGCGCGGTGAATCTTTCGCGGTGTCTGACCGCGAAAGAGCGCAAGCGC	490	500	510	520	530	540	550	560	570	580	590
CGGTGGCAGTTATTCACGCGAGATGGCCGTTTCGGCTAGTGTTCGCGCGCTTTCGCGCTCACCCGCGGCACTTAGGAAAGCGCACGAGCTGGCGCTTTTCTCCGCTTCCG	490	500	510	520	530	540	550	560	570	580	590
A T V N K V R S T G K R I I K A A Q I N G E W G P V N P F G V L D R E K E A K A	490	500	510	520	530	540	550	560	570	580	590
610	620	630	640	650	660	670	680	690	700	710	720
GAGCGCTCACGCTGACGACGAGGTGCGGGGGTCTCCGCGACTTCGCGCGGACCGGCGCGCGAGTTCTCTCCAGTCTTTCGGGCGCACGCCCGCGGAGAGAGAGCG	610	620	630	640	650	660	670	680	690	700	710
CTCGCGAGTGGACTGCGCTCGCTCACGCGCGCGCACGAGCGCTGGAAGCGCGCTGCGCGCGCTCAAGAGAGAGTCCAGAAAGACCCCGGTGCGGCGCGCTTCTCTTCCGCG	610	620	630	640	650	660	670	680	690	700	710
E R L T L T A A E C R A V L P H F R A D R R R E F L F Q V F L G P R P G E E K A	610	620	630	640	650	660	670	680	690	700	710
730	740	750	760	770	780	790	800	810	820	830	840
CTCCTCAAGGAAGATGTGACGTTCGAGGCGCGCACCGTCAATTTTCGGCGCAACAATGTGACGAGACACGAACAAGACGGAACGCGTTCGCGTCCGCGTCCGGAATGATTGTGGCCC	730	740	750	760	770	780	790	800	810	820	830
GAGAGATTCTCTACACCTCAGCTCCGCGCGTGGCAGTAAAGGCGCGCTGTACCTGCTCTGTCTTTCGCCCTCGCTCGCGCGCACGCGCTTCTCAACACCGGG	730	740	750	760	770	780	790	800	810	820	830
L L K E D V D V E A R T V I F R R S N G R D T T K T G R E R R V P V P D E L W P	730	740	750	760	770	780	790	800	810	820	830
850	860	870	880	890	900	910	920	930	940	950	960
GTGCTCTCGATGCGAGCGCAGTCCGCTGTACCTCGTTTCCGAAACGGGAAGGTGAGAGCGCGCGCACGAAGAATGACGCGCTGTGCGCACTGCGCTATCCGCGGCT	850	860	870	880	890	900	910	920	930	940	950
CACGAGAGCTACGCTACGTCGGGTACGAGACAT											

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1090 1100 1110 1120 1130 1140 1150 1160 1170 1180 1190 1200
AGTGTGCGCCCAAAACCCGCGTGTGTACGGGCTCCGTACACCGCGCGACACTGCACAGGAAGCGGGTGCACCGGTCTGTATCAAGCTGTGTGGGGATCGCGTGTGAC
TCACAGCGGGGTTGGCGGCGACACCATGCGCGAGGAGTGTGGCGCGCTGTGACGTGTCTTCGCGCGACCGTGGCGGAGCACTAGTTCGAGCACGACCCCGCTACGCGACAGCTG
S G R P K P A V W Y G L R H T A A T L H R K A G C D P L V I K L V L G H A A V D

1210 1220 1230 1240 1250 1260 1270 1280 1290 1300 1310 1320
ACCACGGACGACGTGTACAGCACTCGACGAGGACTACTGCCGCGCGAACTTAACAAGTTGTGTAAGCCCGCGCCACCACTACTCACAGGAGGAAGTACGGCGGCCTT
TGGTCCCTGCTGCATGTGCGTGGAGCTGCTCCTGATGACGCGCGCGCTTGAATTGTTCAACAGCGCACTTCGGGGGCGGTGTGTGATGAGTGTCCCTTCACTGCGCGCGGA
T T D D V Y T H L D E D Y C R A E L N K L S L K A P P P P T H Q G S D G G P

1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430 1440
GACTCAGGACGCAACCTACGGTGAAGGAGGACCATGCAACGATTGGGAGATTGGCAGCATCACCGGCGGAGAGCTTGGGAAGCTCGTGTCTTACCAACTGAGCTACCAACCGCGGAAC
CTGAGTCTCGGTTGTGGATGCCACTTCCTCCGTGTACGTGCTAACCTCTAAACGTGTAAGTGGCCGCTCTCGAACCCCTTCGAGCACCGAGTGGTTGACTCGATGGTGGCGCTTG
D S G R N T Y G E G G T M H G L G D L Q H R A R A W E A R A L P T E L P P R N

1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560
TTGGCGGGGGTATACCGGCGCGCTGTGAGCGTCAAGGACGTTGCGGCTTCACTCTCAGTGAGCACGGCGAAGGTGTACCACTCTCGCGCGCGCTCCTGCTACCGTGTGGTG
AACCGGCCCCATATGGCGCGGCGACGACTCGCAGTTCTCTGCAACGCGGAAGTGAAGTCACTGTGCGCGCTTCCATGTCGAGGAGCGCGCGCGGAGGACGGATGGCACACCCAC
L A G G I P A P L L S V K D V A A S L S V S T A K V Y Q L L A A G V L P T V W V

1570 1580 1590 1600 1610 1620 1630 1640
GGCCAGTCGCGCCGCTCAAGCGTGAAGGACCTGACCGCTACATCGCCGCGCGACCGCCACCGCGGGAAGCGGGTGGCAATGA
CCGGTCAGCGCGCGAGTTCGACTCCTGGACCTGCGGATGTAGCGGCGCGCTGCCGCTGCGCGCTTCGCCCCACCGTTTACT
G Q S R R V K R E D L D A Y I A R A T A T G G K R G G K *

Figure 3

A.

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10      20      30      40      50      60      70      80      90      100     110     120
GTGAGCTGACCTCAACGGTTTGTGGTGGGAGCGGACAGCGGACCAACATGTGTCAGGGCTTACGGCTTCGCACACGGGGCTGGGCGATGCTGAACGGAGCGTCCCATGTCCACCGG
CACTCGACTGGAGTTGCCAAACACCCACCCCTCGCCCTGTGCTGTGTACCAAGGTGTCGCCGACCCGCTACGACTTGCCTCGCAGGTACAGGTGGCGC

130     140     150     160     170     180     190     200     210     220     230     240
ATGCCGCTGCTTGACATAGGGATTGAAACCTCGAACCCGAGCTTGGGAAGCTCGTCTCTACCAACTGAGCTACCAACGAGGCGAAGCAGGGCGCAAAAGTACGGGCCCGCCCTGTG
TACGGCGGACCGAACGTGTATCCCTAAGCTTTGGAGCTGGGGCTCGAACCCCTTCGAGCAGAGATGGTTGACTCGATGGTGGGCTTCGCTTCGCCGGTTTCATGCCCCGGCGGGACAC

250     260     270     280     290     300     310     320     330     340     350     360
GCTTGTCAAACGGGAAGTGAGTGCTACTCCGTCTCCTCGACGGTGAGCTGGTACGAGTCCTTGGAACTTGGACTCGCGGTTGCGCGCGTCCCGGACCTCGAAGAGGTAGACGCCCTGGCTCG
CGAACAGTTGCCCTTCACCTCACATGAGGCAGAGAGCTGCCACTCGACCATGCTCAGGACCTTCAACCTGAGCGCCAAACGCGCGCAGGGCCTGGAGCTTCTCCATCTGCGGACCGGAGC
```

B.

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10      20      30      40      50      60      70      80      90      100     110     120
CGAGCCGGGACGGGAGCGGGGACCGGCTTCGCGCCGTTTACAGCATCCTTGTCTCAAGACGCCCCGAGGCGCGAAAGACGAAGGCGCGGAGTCCCGAGTTTCTCAAGGACTACCG
GCTCGGCCCTGCCCCCTGGCCGGAAGCGCGGCAAAATGTGCTAGGAACGACGTTCTCGGGGCTCCGGGCTTTCTGCTTCCGGCCGTCAGGCTCAAAGGAGTTCTCTGATGGC

130     140     150     160     170     180     190     200     210     220     230     240
GCCTTCATGGGTGAGCGGCGGAAGGATTCGAACCCCTCGACCCCGAGCTTGGGAAGCTTCGTCTTACCAACTGAGCTACCAACGAGGCGAAGTACGGGGCGCCCTG
CGGAAGTACCCACTCGCCGCCCTTCCCTAAGCTTGGAGCTGGGGCTCGAACCTTGGAGACGAGATGGTTGACTCGATGGTGGGCTTCGCTTCGCCCGTTTCATGCCCGCGGGGAC

250     260     270     280     290     300     310     320     330     340     350     360
TGGCTTGTCAACGGGAAGTGAGGTGCTACTCCGTCTCCTCGACGGTGAGCTGGTACGAGTCTCGGAAGTTGGACTCGCGGTTGGCGCGCTCCCGACCTCGAAGAGGTAGACGCTGGCT
ACCGAACAGTTGCCCTTCACCTCACATGAGGCAGAGAGCTGCCACTCGACCATGCTCAGGACCTTCAACCTGAGCGCCAAACGCGCGCAGGGCCTGGAGCTTCTCCATCTGCGGACCGGA
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C.

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10 20 30 40 50 60 70 80 90 100 110 120
TGCAGGGCTTACGGCTTCGCACACGGGGCTGGCGATGCTGAACGGAGCGTCCCATGTCCACGCGATGCGCCTGGCTTGACATAGGGAATTCGAAACCTTCGACCCCGAGCTTGGGAAG
ACGGTCCCGAATGCCGAAGCGTGTGCCCCGACCGCTACGACTTGCCTCGCAGGGTACAGGTGCGCTACGGCGGACCGAACGTGTATCCCTAAGCTTTGGAGCTGGGGCTCGAACCCCTTC
130 140 150 160 170 180 190 200 210 220 230 240
CTCGGCCTCGACCCGTCAGGCGTTATCAGCCGTTTCGCAACCCCTTACTTCGCCCTTGGGATTCGGGGCGGGGCGCTGTCCATCCGTCGACGCGGTAGCAGGGAGTCTCAGGGGGGTT
GAGCCGAGCTGGGCAGGTCCGCAATAGTCGGCAAGCGTTTGGGAATGAACGGNAACCCCTAAGCCCCGGCCCCCGGACAGGTAGGCAGGTCGCCCATCGTCCCTCAGAGTCCCCCCCA
```

D.

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10 20 30 40 50 60 70 80 90 100 110 120
CGCCACCACTACTACAGGAGGAGTGAACGGGGCCCTGACTCAGGAGCGAACAACCTACGGTGAAGGAGGACCATGCACGGATTGGGAGATTGGAGCATCACCGGGCGAGAGCTT
GCGGTGGTGATGAGTGGTCCCTTCACTGCGCGCGGACTGAGTCCCTGCTGTGGATGCCACTTCCTCCGTGTAGTGCTAACCCCTCTAAACGTCGTAGTGGCCGCTCTCGAA
130 140 150 160 170 180 190 200 210 220 230 240
GGGAAGCTCGTGTCTTACCAACTGAGCTACACCGCGGAACCTTGGCCGGGGGTATACCGGCGCCGCTGCTGAGCGTCAAGGACGTTGGGCTTCACTCTCAGTGAGCAGCGGCGAAGGTGT
CCCTTCGAGCAGAGATGGTTGACTCGATGGTGGCGCTTGAAACCGGCCCCCATATGGCGCGGCGACGACTCGCAGTTCCTGCAACCGCGGAAGTGAGAGTCACTCGTCCGCTTCCACA
→
250
ACGAGCTCCTCGCCGCG
TGGTCGAGGAGCGGCGG
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The diagram illustrates the cloverleaf secondary structure of a tRNA molecule. The structure is composed of several stems and loops. The acceptor arm at the top has a 3' terminal CCA sequence. The D arm contains a dihydrouridine (D) loop. The anticodon arm at the bottom contains an anticodon loop with the anticodon sequence UCC. The T arm contains a thymine (T) loop. The variable arm is at the right. Nucleotides are represented by letters A, C, G, U.

Figure 4

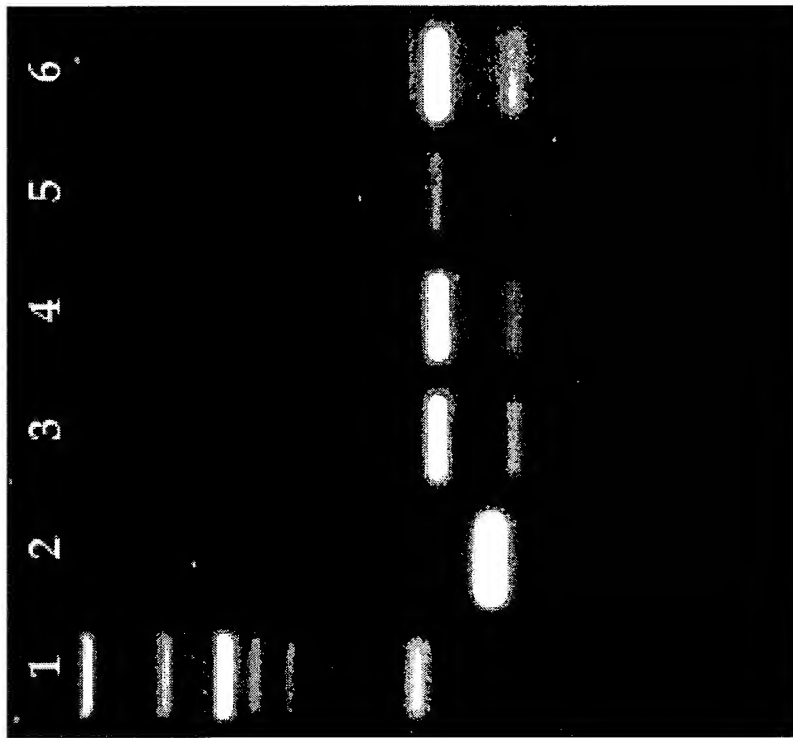


FIGURE 5

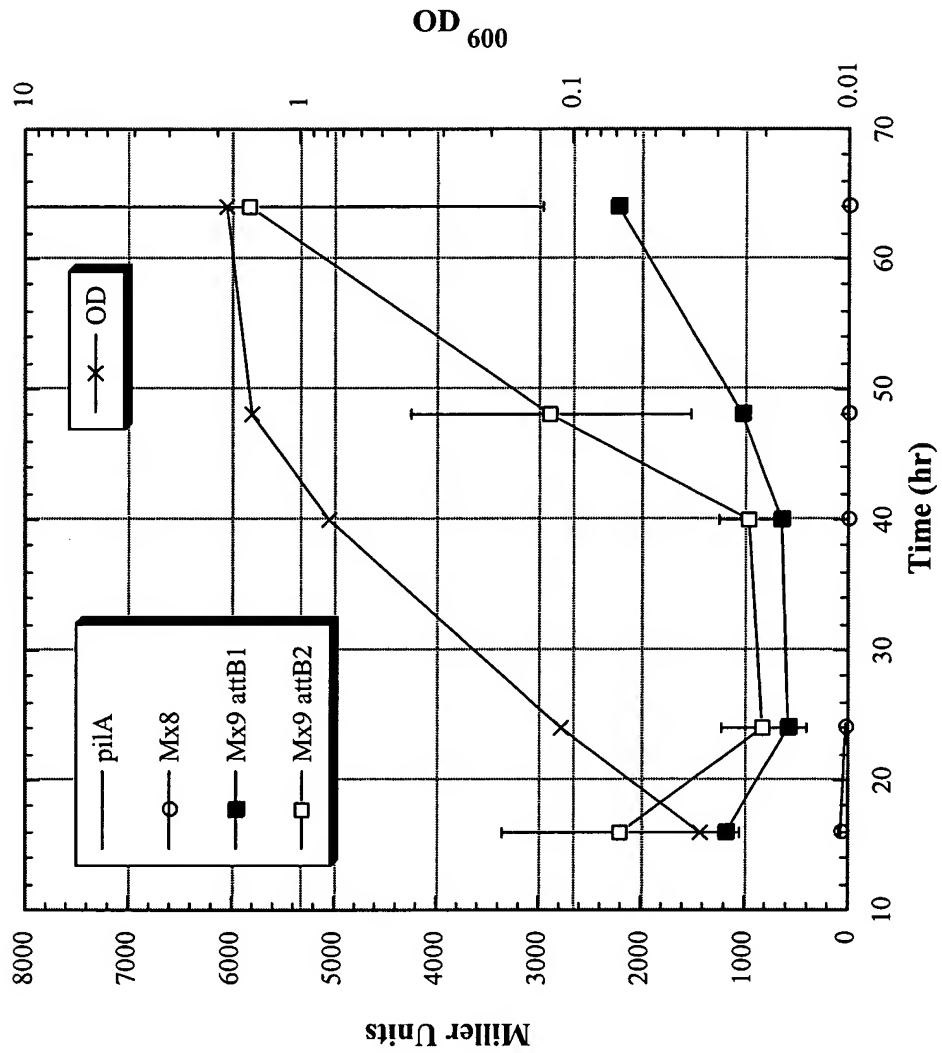


FIGURE 6A

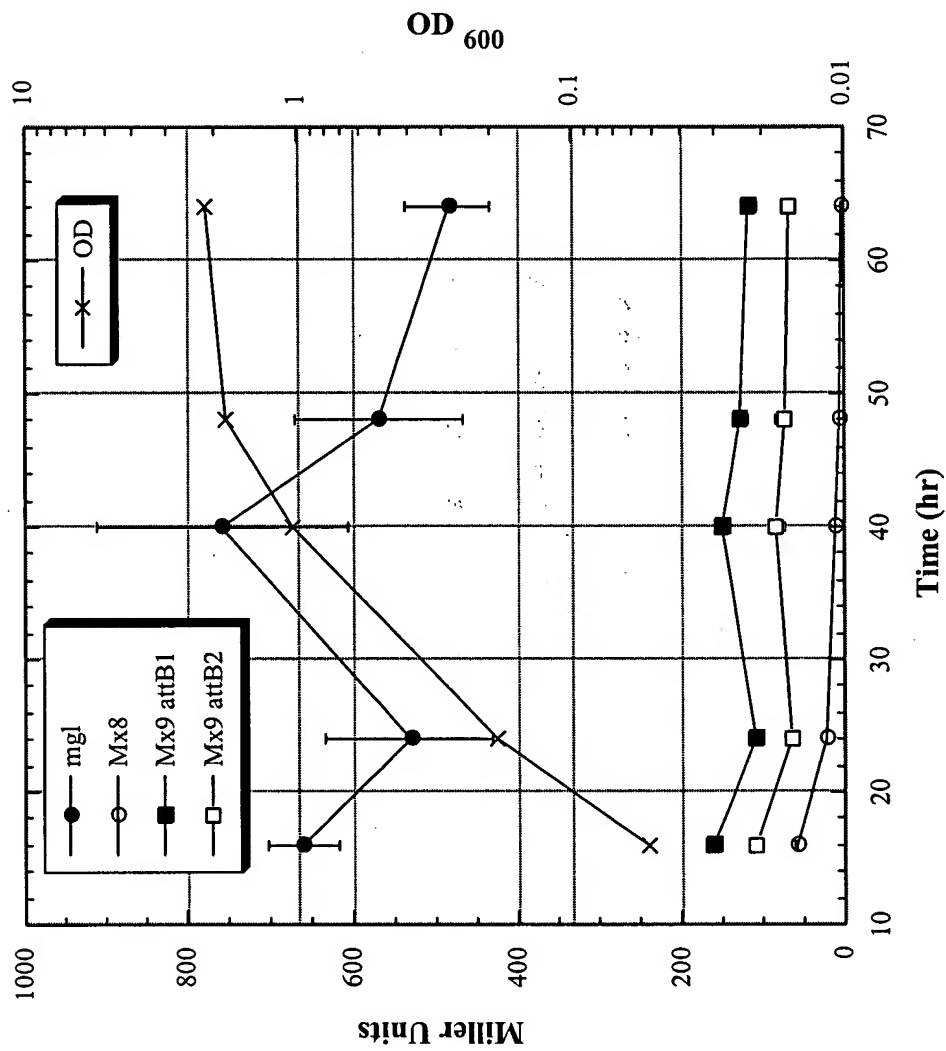


FIGURE 6B

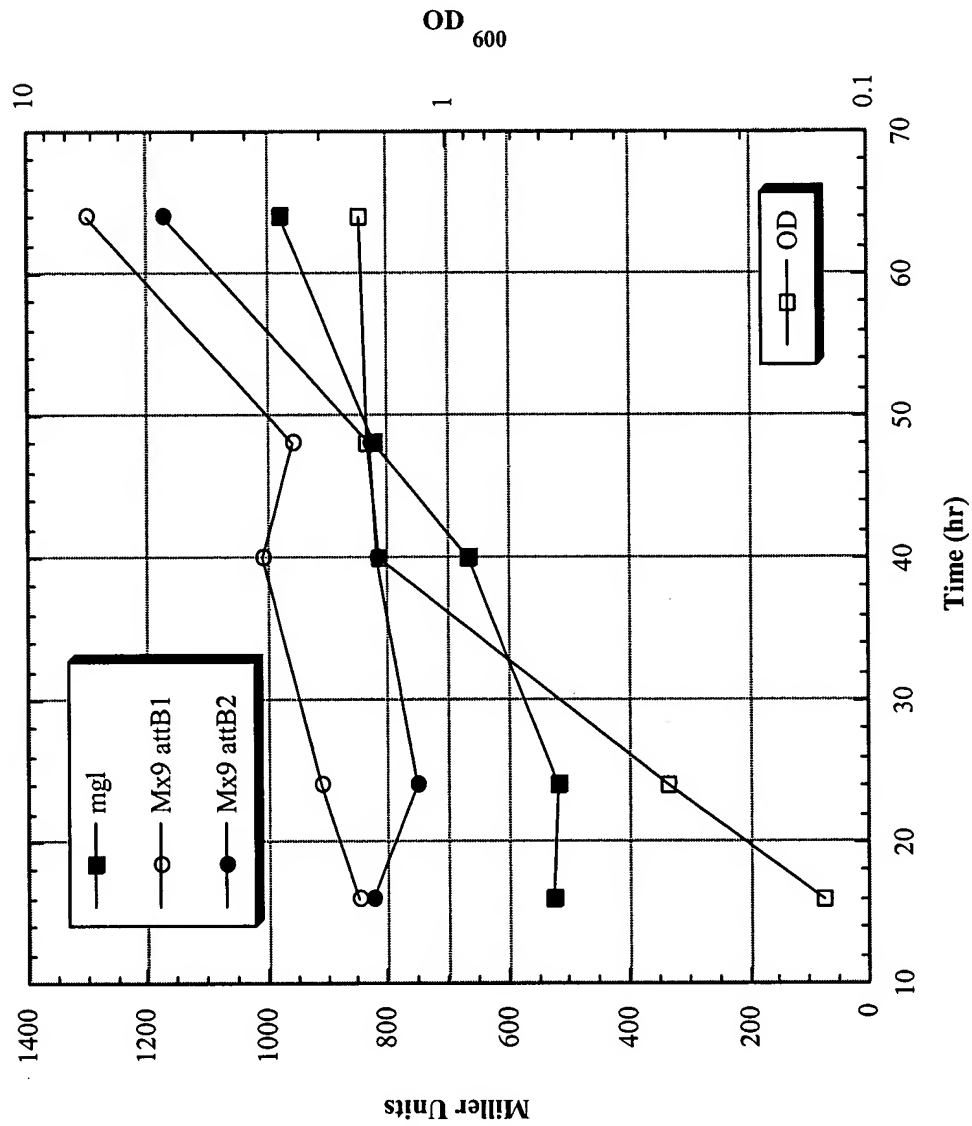


FIGURE 6C

Figure 7

10	20	30	40	50	60
ATG GAA AAA AAG	GAA TTT CGT GTT	TTG ATA AAA TAC	TGT TTT CTG AAG	GGA AAA AAT ACA	
TAC CTT TTT TTC	CTT AAA GCA CAA	AAC TAT TTT ATG	ACA AAA GAC TTC	CCT TTT TTA TGT	
Met Glu Lys Lys	Glu Asn Arg Val	Leu Ile Lys Tyr	Cys Asn Leu Lys	Gly Lys Asn Thr	
70	80	90	100	110	120
GTG GAA GCA AAA	ACT TGG CTT GAT	AAT GAG TTT CCG	GAC TCT GCC CCA	GGG AAA TCA ACA	
CAC CTT CGT TTT	TGA ACC GAA CTA	TTA CTC AAA GGC	CTG AGA CGG GGT	CCC TTT AGT TGT	
Val Glu Ala Lys	Thr Trp Leu Asp	Asn Glu Asn Pro	Asp Ser Ala Pro	Gly Lys Ser Thr	
130	140	150	160	170	180
ATA ATT GAT TGG	TAT GCA AAA TTC	AAG CGT GGT GAA	ATG AGC ACG GAG	GAC GGT GAA CGC	
TAT TAA CTA ACC	ATA CGT TTT AAG	TTC GCA CCA CTT	TAC TCG TGC CTC	CTG CCA CTT GCG	
Ile Ile Asp Trp	Tyr Ala Lys Phe	Lys Arg Gly Glu	Met Ser Thr Glu	Asp Gly Glu Arg	
190	200	210	220	230	240
AGT GGA CGC CCG	AAA GAG GTG GTT	ACC GAC GAA AAC	ATC AAA AAA ATC	CAC AAA ATG ATT	
TCA CCT GCG GGC	TTT CTC CAC CAA	TGG CTG CTT TTG	TAG TTT TTT TAG	GTG TTT TAC TAA	
Ser Gly Arg Pro	Lys Glu Val Val	Thr Asp Glu Asn	Ile Lys Lys Ile	His Lys Met Ile	
250	260	270	280	290	300
TTG AAT GAC CGT	AAA ATG AAG TTG	ATC GAG ATA GCA	GAG GCC TTA AAG	ATA TCA AAG GAA	
AAC TTA CTG GCA	TTT TAC TTC AAC	TAG CTC TAT CGT	CTC CGG AAT TTC	TAT AGT TTC CTT	
Leu Asn Asp Arg	Lys Met Lys Leu	Ile Glu Ile Ala	Glu Ala Leu Lys	Ile Ser Lys Glu	
310	320	330	340	350	360
CGT GTT GGT CAT	ATC ATT CAT CAA	TAT TTG GAT ATG	CGG AAG CTC TGT	GCA AAA TGG GTG	
GCA CAA CCA GTA	TAG TAA GTA GTT	ATA AAC CTA TAC	GCC TTC GAG ACA	CGT TTT ACC CAC	
Arg Val Gly His	Ile Ile His Gln	Tyr Leu Asp Met	Arg Lys Leu Cys	Ala Lys Trp Val	
370	380	390	400	410	420
CCG CGC GAG CTC	ACA TTT GAC CAA	AAA CAA CAA CGT	GTT GAT GAT TCT	GAG CGG TGT TTG	
GGC GCG CTC GAG	TGT AAA CTG GTT	TTT GTT GTT GCA	CAA CTA CTA AGA	CTC GCC ACA AAC	
Pro Arg Glu Leu	Thr Asn Asp Gln	Lys Gln Gln Arg	Val Asp Asp Ser	Glu Arg Cys Leu	
430	440	450	460	470	480
CAG CTG TTA ACT	CGT AAT ACA CCC	GAG TTT TTC CGT	CGA TAT GTG ACA	ATG GAT GAA ACA	
GTC GAC AAT TGA	GCA TTA TGT GGG	CTC AAA AAG GCA	GCT ATA CAC TGT	TAC CTA CTT TGT	
Gln Leu Leu Thr	Arg Asn Thr Pro	Glu Asn Phe Arg	Arg Tyr Val Thr	Met Asp Glu Thr	
490	500	510	520	530	540
TGG CTC CAT CAC	TAC ACT CCT GAG	TCC AAT CGA CAG	TCG GCT GAG TGG	ACA GCG ACC GGT	
ACC GAG GTA GTG	ATG TGA GGA CTC	AGG TTA GCT GTC	AGC CGA CTC ACC	TGT CGC TGG CCA	
Trp Leu His His	Tyr Thr Pro Glu	Ser Asn Arg Gln	Ser Ala Glu Trp	Thr Ala Thr Gly	
550	560	570	580	590	600
GAA CCG TCT CCG	AAG CGT GGA AAG	ACT CAA AAG TCC	GCT GGC AAA GTA	ATG GCC TCT GTT	
CTT GGC AGA GGC	TTC GCA CCT TTC	TGA GTT TTC AGG	CGA CCG TTT CAT	TAC CGG AGA CAA	
Glu Pro Ser Pro	Lys Arg Gly Lys	Thr Gln Lys Ser	Ala Gly Lys Val	Met Ala Ser Val	

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610	620	630	640	650	660
TTT TTC GAT GCG CAT GGA ATA ATT TTT ATC GAT TAT CTT GAG AAG GGA AAA ACC ATC AAC					
AAA AAG CTA CGC GTA CCT TAT TAA AAA TAG CTA ATA GAA CTC TTC CCT TTT TGG TAG TTG					
Asn Phe Asp Ala His Gly Ile Ile Asn Ile Asp Tyr Leu Glu Lys Gly Lys Thr Ile Asn					
670	680	690	700	710	720
AGT GAC TAT TAT ATG GCG TTA TTG GAG CGT TTG AAG GTC GAA ATC GCG GCA AAA CGG CCC					
TCA CTG ATA ATA TAC CGC AAT AAC CTC GCA AAC TTC CAG CTT TAG CGC CGT TTT GCC GGG					
Ser Asp Tyr Tyr Met Ala Leu Leu Glu Arg Leu Lys Val Glu Ile Ala Ala Lys Arg Pro					
730	740	750	760	770	780
CAT ATG AAG AAG AAA AAA GTG TTG TTC CAC CAA GAC AAC GCA CCG TGC CAC AAG TCA TTG					
GTA TAC TTC TTC TTT TTT CAC AAC AAG GTG GTT CTG TTG CGT GGC ACG GTG TTC AGT AAC					
His Met Lys Lys Lys Lys Val Leu Phe His Gln Asp Asn Ala Pro Cys His Lys Ser Leu					
790	800	810	820	830	840
AGA ACG ATG GCA AAA ATT CAT GAA TTG GGC TTC GAA TTG CTT CCC CAC CCA CCG TAT TCT					
TCT TGC TAC CGT TTT TAA GTA CTT AAC CCG AAG CTT AAC GAA GGG GTG GGT GGC ATA AGA					
Arg Thr Met Ala Lys Ile His Glu Leu Gly Phe Glu Leu Leu Pro His Pro Pro Tyr Ser					
850	860	870	880	890	900
CCA GAT CTG GCC CCC AGC GAC TTT TTC TTG TTC TCA GAC CTC AAA AGG ATG CTC GCA GGG					
GGT CTA GAC CGG GGG TCG CTG AAA AAG AAC AAG AGT CTG GAG TTT TCC TAC GAG CGT CCC					
Pro Asp Leu Ala Pro Ser Asp Asn Phe Leu Phe Ser Asp Leu Lys Arg Met Leu Ala Gly					
910	920	930	940	950	960
AAA AAA TTT GGC TGC AAT GAA GAG GTG ATC GCC GAA ACT GAG GCC TAT TTT GAG GCA AAA					
TTT TTT AAA CCG ACG TTA CTT CTC CAC TAG CGG CTT TGA CTC CGG ATA AAA CTC CGT TTT					
Lys Lys Asn Gly Cys Asn Glu Glu Val Ile Ala Glu Thr Glu Ala Tyr Asn Glu Ala Lys					
970	980	990	1000	1010	1020
CCG AAG GAG TAC TAC CAA AAT GGT ATC AAA AAA TTG GAA GGT CGT TAT AAT CGT TGT ATC					
GGC TTC CTC ATG ATG GTT TTA CCA TAG TTT TTT AAC CTT CCA GCA ATA TTA GCA ACA TAG					
Pro Lys Glu Tyr Tyr Gln Asn Gly Ile Lys Lys Leu Glu Gly Arg Tyr Asn Arg Cys Ile					
1030	1040				
GCT CTT GAA GGG AAC TAT GTT GAA TAA					
CGA GAA CTT CCC TTG ATA CAA CTT ATT					
Ala Leu Glu Gly Asn Tyr Val Glu ***					